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## RAW SEQUENCE LISTING

DATE: 02/22/2002

PATENT APPLICATION: US/10/007,010

TIME: 15:39:27

Input Set : A:\RTS-0345 Sequence Listing.txt

Output Set: N:\CRF3\02222002\J007010.raw

# 2

```

3 <110> APPLICANT: Alexander H. Borchers
4   Kenneth W. Dobie
6 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF HCK EXPRESSION
8 <130> FILE REFERENCE: RTS-0345
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/007,010
C--> 10 <141> CURRENT FILING DATE: 2001-12-04
10 <160> NUMBER OF SEQ ID NOS: 87
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 20
15 <212> TYPE: DNA
16 <213> ORGANISM: Artificial Sequence
18 <220> FEATURE:
20 <223> OTHER INFORMATION: Antisense Oligonucleotide
22 <400> SEQUENCE: 1
23 tccgtcatcg ctctcaggg                                20
26 <210> SEQ ID NO: 2
27 <211> LENGTH: 20
28 <212> TYPE: DNA
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
33 <223> OTHER INFORMATION: Antisense Oligonucleotide
35 <400> SEQUENCE: 2
36 atgcattctg cccccaagga                                20
39 <210> SEQ ID NO: 3
40 <211> LENGTH: 2015
41 <212> TYPE: DNA
42 <213> ORGANISM: Homo sapiens
44 <220> FEATURE:
46 <221> NAME/KEY: CDS
47 <222> LOCATION: (169)...(1686)
49 <400> SEQUENCE: 3
50 cggaggcacg gaagatgagg aagatgatca ggaggatgat gaaggtgaag agggagatga    60
52 agacgatgac gacgatggct ctgaggggac ctcaggggct gccgagctgg gggggcgctc    120
54 aagctgcgag gatccgggct gcccgcgaga cgaggagcgg gcgccagg atg ggg tcg    177
55                                     Met Gly Ser
56                                     1
58 atg aag tcc aag ttc ctc cag gtc gga ggc aat aca ttc tca aaa act    225
59 Met Lys Ser Lys Phe Leu Gln Val Gly Gly Asn Thr Phe Ser Lys Thr
60   5          10          15
62 gaa acc agc gcc agc cca cac tgt cct gtg tac gtg ccg gat ccc aca    273
63 Glu Thr Ser Ala Ser Pro His Cys Pro Val Tyr Val Pro Asp Pro Thr
64 20          25          30          35
66 tcc acc atc aag ccg ggg cct aat agc cac aac agc aac aca cca gga    321

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```

67 Ser Thr Ile Lys Pro Gly Pro Asn Ser His Asn Ser Asn Thr Pro Gly
68          40          45          50
70 atc agg gag gca ggc tct gag gac atc atc gtg gtt gcc ctg tat gat      369
71 Ile Arg Glu Ala Gly Ser Glu Asp Ile Ile Val Val Ala Leu Tyr Asp
72          55          60          65
74 tac gag gcc att cac cac gaa gac ctc agc ttc cag aag ggg gac cag      417
75 Tyr Glu Ala Ile His His Glu Asp Leu Ser Phe Gln Lys Gly Asp Gln
76          70          75          80
78 atg gtg gtc cta gag gaa tcc ggg gag tgg tgg aag gct cga tcc ctg      465
79 Met Val Val Leu Glu Glu Ser Gly Glu Trp Trp Lys Ala Arg Ser Leu
80          85          90          95
82 gcc acc cgg aag gag ggc tac atc cca agc aac tat gtc gcc cgc gtt      513
83 Ala Thr Arg Lys Glu Gly Tyr Ile Pro Ser Asn Tyr Val Ala Arg Val
84 100          105          110          115
86 gac tct ctg gag aca gag gag tgg ttt ttc aag ggc atc agc cgg aag      561
87 Asp Ser Leu Glu Thr Glu Glu Trp Phe Phe Lys Gly Ile Ser Arg Lys
88          120          125          130
90 gac gca gag cgc caa ctg ctg gct ccc ggc aac atg ctg ggc tcc ttc      609
91 Asp Ala Glu Arg Gln Leu Leu Ala Pro Gly Asn Met Leu Gly Ser Phe
92          135          140          145
94 atg atc cgg gat agc gag acc act aaa gga agc tac tct ttg tcc gtg      657
95 Met Ile Arg Asp Ser Glu Thr Thr Lys Gly Ser Tyr Ser Leu Ser Val
96          150          155          160
98 cga gac tac gac cct cgg cag gga gat acc gtg aaa cat tac aag atc      705
99 Arg Asp Tyr Asp Pro Arg Gln Gly Asp Thr Val Lys His Tyr Lys Ile
100          165          170          175
102 cgg acc ctg gac aac ggg ggc ttc tac ata tcc ccc cga agc acc ttc      753
103 Arg Thr Leu Asp Asn Gly Gly Phe Tyr Ile Ser Pro Arg Ser Thr Phe
104 180          185          190          195
106 agc act ctg cag gag ctg gtg gac cac tac aag aag ggg aac gac ggg      801
107 Ser Thr Leu Gln Glu Leu Val Asp His Tyr Lys Lys Gly Asn Asp Gly
108          200          205          210
110 ctc tgc cag aaa ctg tcg gtg ccc tgc atg tct tcc aag ccc cag aag      849
111 Leu Cys Gln Lys Leu Ser Val Pro Cys Met Ser Ser Lys Pro Gln Lys
112          215          220          225
114 cct tgg gag aaa gat gcc tgg gag atc cct cgg gaa tcc ctc aag ctg      897
115 Pro Trp Glu Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Lys Leu
116          230          235          240
118 gag aag aaa ctt gga gct ggg cag ttt ggg gaa gtc tgg atg gcc acc      945
119 Glu Lys Lys Leu Gly Ala Gly Gln Phe Gly Glu Val Trp Met Ala Thr
120          245          250          255
122 tac aac aag cac acc aag gtg gca gtg aag acg atg aag cca ggg agc      993
123 Tyr Asn Lys His Thr Lys Val Ala Val Lys Thr Met Lys Pro Gly Ser
124 260          265          270          275
126 atg tcg gtg gag gcc ttc ctg gca gag gcc aac gtg atg aaa act ctg      1041
127 Met Ser Val Glu Ala Phe Leu Ala Glu Ala Asn Val Met Lys Thr Leu
128          280          285          290
130 cag cat gac aag ctg gtc aaa ctt cat gcg gtg gtc acc aag gag ccc      1089
131 Gln His Asp Lys Leu Val Lys Leu His Ala Val Val Thr Lys Glu Pro

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```

132          295          300          305
134 atc tac atc atc acg gag ttc atg gcc aaa gga agc ttg ctg gac ttt 1137
135 Ile Tyr Ile Ile Thr Glu Phe Met Ala Lys Gly Ser Leu Leu Asp Phe
136          310          315          320
138 ctg aaa agt gat gag ggc agc aag cag cca ttg cca aaa ctc att gac 1185
139 Leu Lys Ser Asp Glu Gly Ser Lys Gln Pro Leu Pro Lys Leu Ile Asp
140          325          330          335
142 ttc tca gcc cag att gca gaa ggc atg gcc ttc atc gag cag agg aac 1233
143 Phe Ser Ala Gln Ile Ala Glu Gly Met Ala Phe Ile Glu Gln Arg Asn
144 340          345          350          355
146 tac atc cac cga gac ctc cga gct gcc aac atc ttg gtc tct gca tcc 1281
147 Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser Ala Ser
148          360          365          370
150 ctg gtg tgt aag att gct gac ttt ggc ctg gcc cgg gtc att gag gac 1329
151 Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Val Ile Glu Asp
152          375          380          385
154 aac gag tac acg gct cgg gaa ggg gcc aag ttc ccc atc aag tgg aca 1377
155 Asn Glu Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile Lys Trp Thr
156          390          395          400
158 gct cct gaa gcc atc aac ttt ggc tcc ttc acc atc aag tca gac gtc 1425
159 Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys Ser Asp Val
160          405          410          415
162 tgg tcc ttt ggt atc ctg ctg atg gag atc gtc acc tac ggc cgg atc 1473
163 Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr Gly Arg Ile
164 420          425          430          435
166 cct tac cca ggg atg tca aac cct gaa gtg atc cga gct ctg gag cgt 1521
167 Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala Leu Glu Arg
168          440          445          450
170 gga tac cgg atg cct cgc cca gag aac tgc cca gag gag ctc tac aac 1569
171 Gly Tyr Arg Met Pro Arg Pro Glu Asn Cys Pro Glu Glu Leu Tyr Asn
172          455          460          465
174 atc atg atg cgc tgc tgg aaa aac cgt ccg gag gag cgg ccg acc ttc 1617
175 Ile Met Met Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg Pro Thr Phe
176          470          475          480
178 gaa tac atc cag agt gtg ctg gat gac ttc tac acg gcc aca gag agc 1665
179 Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala Thr Glu Ser
180          485          490          495
182 cag tac caa cag cag cca tga tagggaggac cagggcaggg caggggggtgc 1716
183 Gln Tyr Gln Gln Gln Pro
184 500          505
186 ccaggtggtg gctcgaaggt ggctccagca ccatccgcca gggcccacac ccccttccta 1776
188 ctcccagaca cccaccctcg cttcagccac agtttctctca tctgtccagt gggtaggttg 1836
190 gactggaaaa tctctttttg actcttgcaa tccacaatct gacattctca ggaagcccc 1896
192 aagttgatat ttctatttcc tggaatggtt ggatttttagt tacagctgtg atttggaagg 1956
194 gaaactttca aaatagttaa atgaatattt aaataaaaaga tataaatgca agtcttacg 2015
197 <210> SEQ ID NO: 4
198 <211> LENGTH: 20
199 <212> TYPE: DNA
200 <213> ORGANISM: Artificial Sequence

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Input Set : A:\RTS-0345 Sequence Listing.txt

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```

202 <220> FEATURE:
204 <223> OTHER INFORMATION: PCR Primer
206 <400> SEQUENCE: 4
207 tttgtccgtg cgagactacg 20
210 <210> SEQ ID NO: 5
211 <211> LENGTH: 19
212 <212> TYPE: DNA
213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
217 <223> OTHER INFORMATION: PCR Primer
219 <400> SEQUENCE: 5
220 ttgtccaggg tccggatct 19
223 <210> SEQ ID NO: 6
224 <211> LENGTH: 29
225 <212> TYPE: DNA
226 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
230 <223> OTHER INFORMATION: PCR Probe
232 <400> SEQUENCE: 6
233 ctccggcaggg agataccgtg aaacattac 29
236 <210> SEQ ID NO: 7
237 <211> LENGTH: 19
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
243 <223> OTHER INFORMATION: PCR Primer
245 <400> SEQUENCE: 7
246 gaaggtgaag gtcggagtc 19
249 <210> SEQ ID NO: 8
250 <211> LENGTH: 20
251 <212> TYPE: DNA
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
256 <223> OTHER INFORMATION: PCR Primer
258 <400> SEQUENCE: 8
259 gaagatggtg atgggatttc 20
262 <210> SEQ ID NO: 9
263 <211> LENGTH: 20
264 <212> TYPE: DNA
265 <213> ORGANISM: Artificial Sequence
267 <220> FEATURE:
269 <223> OTHER INFORMATION: PCR Probe
271 <400> SEQUENCE: 9
272 caagcttccc gttctcagcc 20
275 <210> SEQ ID NO: 10
276 <211> LENGTH: 30000
277 <212> TYPE: DNA
278 <213> ORGANISM: Homo sapiens
280 <220> FEATURE:

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Input Set : A:\RTS-0345 Sequence Listing.txt

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282 <221> NAME/KEY: exon  
283 <222> LOCATION: (4334)...(4437)  
284 <223> OTHER INFORMATION: exon 5  
W--> 286 <221> NAME/KEY: exon:intron junction  
287 <222> LOCATION: (4437)...(4438)  
288 <223> OTHER INFORMATION: exon 5:intron 5  
290 <221> NAME/KEY: intron  
291 <222> LOCATION: (4438)...(8453)  
292 <223> OTHER INFORMATION: intron 5  
W--> 294 <221> NAME/KEY: intron:exon junction  
295 <222> LOCATION: (8453)...(8454)  
296 <223> OTHER INFORMATION: intron 5:exon 6  
298 <221> NAME/KEY: exon  
299 <222> LOCATION: (8454)...(8603)  
300 <223> OTHER INFORMATION: exon 6  
W--> 302 <221> NAME/KEY: exon:intron junction  
303 <222> LOCATION: (8603)...(8604)  
304 <223> OTHER INFORMATION: exon 6:intron 6  
W--> 306 <221> NAME/KEY: intron:exon junction  
307 <222> LOCATION: (8950)...(8951)  
308 <223> OTHER INFORMATION: intron 6:exon 7  
310 <221> NAME/KEY: exon  
311 <222> LOCATION: (8951)...(9103)  
312 <223> OTHER INFORMATION: exon 7  
W--> 314 <221> NAME/KEY: exon:intron junction  
315 <222> LOCATION: (9103)...(9104)  
316 <223> OTHER INFORMATION: exon 7:intron 7  
318 <221> NAME/KEY: intron  
319 <222> LOCATION: (9104)...(11187)  
320 <223> OTHER INFORMATION: intron 7  
W--> 322 <221> NAME/KEY: intron:exon junction  
323 <222> LOCATION: (11187)...(11188)  
324 <223> OTHER INFORMATION: intron 7:exon 8  
326 <221> NAME/KEY: exon  
327 <222> LOCATION: (11188)...(11367)  
328 <223> OTHER INFORMATION: exon 8  
W--> 330 <221> NAME/KEY: exon:intron junction  
331 <222> LOCATION: (11367)...(11368)  
332 <223> OTHER INFORMATION: exon 8:intron 8  
334 <221> NAME/KEY: intron  
335 <222> LOCATION: (11368)...(13127)  
336 <223> OTHER INFORMATION: intron 8  
W--> 338 <221> NAME/KEY: intron:exon junction  
339 <222> LOCATION: (13127)...(13128)  
340 <223> OTHER INFORMATION: intron 8:exon 9  
342 <221> NAME/KEY: exon  
343 <222> LOCATION: (13128)...(13204)  
344 <223> OTHER INFORMATION: exon 9  
W--> 346 <221> NAME/KEY: exon:intron junction

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/007,010

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Input Set : A:\RTS-0345 Sequence Listing.txt

Output Set: N:\CRF3\02222002\J007010.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:286 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:294 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:302 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:306 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:314 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:322 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:330 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:338 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:346 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:354 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:362 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:370 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:378 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:386 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10